



SEQUENCE LISTING

<110> KRIMMER, HANS-PETER
MAY, OLIVER
KLEMENT, INGO
DRAUZ, KARLHEINZ
REICHERT, DIETMAR

<120> PROCESS FOR THE PREPARATION OF ALLYSINE ACETAL

<130> 210740US0X

<140> 09/916,501

<141> 2001-07-30

<150> DE 100 37 115.9

<151> 2000-07-28

<160> 24

<170> PatentIn version 3.1

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<211> 1377

<212> DNA

<213> Arthrobacter aurescens

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 <212> DNA
 <213> *Arthrobacter aurescens*

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<211> 1239

<212> DNA

<213> Arthrobacter aurescens

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cggaaacgc tcattgcggc tatgaaagcg gccgccttga gcgttcgtga agacgcactc 180

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gccattgcag gtttggtcgc cgacaggaa ctggactctt tggatgtca ggtggagtg 480

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gagcaggagc aaatagagat cggagttgtac acctccatcg ttggcggtcg cgattgcgg 660

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gcgctggta cggccgctct catggtgagg gaggtcaacc gttcgtcaa cgagatgcc 780

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cacgactcga tggatcgac ccaggtcactg gacgtcgaa tggtttcgt tccaagccgt 1140

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gaggttgcc tccggtaat gaaggcactt gaccggtaa 1239

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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic DNA

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<212> DNA
<213> *Arthrobacter aurescens*

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<210> 6
<211> 1263
<212> DNA
<213> *Arthrobacter aurescens*

<220>
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<222> (25)..(25)
<223> n = any nucleotide

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<210> 7
 <211> 1377
 <212> DNA
 <213> *Arthrobacter* sp.

<400> 7
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<210> 8
 <211> 458
 <212> PRT
 <213> Arthrobacter sp.

<400> 8

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20 25 30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr
85 90 95

Phe Pro Pro Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr

195

200

205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
420 425 430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
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Val Thr Arg His Asp Tyr Glu Ala Ser Lys
450 455

<210> 9
<211> 1377
<212> DNA
<213> Arthrobacter sp.

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<210> 10

<211> 458

<212> PRT

<213> Arthrobacter sp.

<400> 10

Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly
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Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
20 25 30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr
85 90 95

Phe Pro Pro Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Ala Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Val Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr
195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp

305	310	315	320
Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu			
325	330	335	
Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys			
340	345	350	
Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro			
355	360	365	
Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly			
370	375	380	
Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val			
385	390	395	400
Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly			
405	410	415	
Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val			
420	425	430	
Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe			
435	440	445	
Val Thr Arg His Asp Tyr Glu Ala Ser Lys			
450	455		
<210> 11			
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<213> Arthrobacter sp.			
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gcgagccgaa ccattgacgc gggtggcaag ttcgtgtatgc cgggcgttgt cgtatgaacat			180

gcgagccgaa	ccattgacgc	gggtggcaag	ttcgtatgc	cggcggttgt	cgatgaacat	240
tctgcggccg	tgggaggcat	caccaccatc	atcgagatgc	cgttaacctt	cccgcccacc	300
accactttgg	acgccttcct	cgaaaagaag	aagcaggcgg	ggcagcggtt	gaaagttgac	360
ttcgcgtct	atggcggtgg	agtgcggga	aacctgcccc	agatccgcaa	aatgcacgac	420
gccggcgcag	tgggcttcaa	gtcaatgatg	gcagcctcag	ttccggcat	gttcgacgcc	480
gtcagcgacg	gcgaactgtt	cgaaatcttc	caggagatcg	cagcctgtgg	ttcagtcgtc	540
gtggtccatg	ccgagaatga	aacgatcatt	caagcgctcc	agaagcagat	caaagccgct	600
ggtcgcaagg	acatggccgc	ctacgaggca	tcccaaccag	tttccagga	gaacgaggcc	660
attcagcgtg	cgttactact	gcagaaagaa	gccggctgtc	gactgattgt	gcttcacgtg	720
agcaaccctg	acggggtcga	gctgatacat	caggcgcaat	ccgagggcca	ggacgtccac	780
tgcgagtcgg	gtccgcagta	tctgaatatc	accacggacg	acgcccgaacg	aatcggaccg	840
tatataagg	tcgcgcgc	cgtccgctca	gccgagatga	acgtcagatt	atggaaaca	900
cttgagaacg	ggctcatcga	cacccttggg	tcagaccacg	gcccacatcc	tgtcgaggac	960
aaagaacccg	gctggaagga	cgtgtggaaa	gccggcaacg	gtgcgttggg	cctttagaca	1020
tccctgccta	tgtgtgtac	caacggagt	aataaaggca	ggctatcctt	ggaacgcctc	1080
gtcgaggtga	tgtgcgagaa	acctgcgaag	ctctttggca	tctatccgca	gaagggcacg	1140
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gatgcctcgc	agttccgatc	cctgcataag	tacagcccgt	tcgacggat	gcccgtcacg	1260
ggtgtcaccgg	ttctgacgat	ggtgcgcgga	acggtggtgg	cagagaaggg	agaagttctg	1320
gtcgagcagg	gattcggcca	gttcgtcacc	cgtcacgact	acgaggcgtc	gaagtga	1377

<210> 12
 <211> 458
 <212> PRT
 <213> *Arthrobacter* sp.
 <400> 12

Met	Phe	Asp	Val	Ile	Val	Lys	Asn	Cys	Arg	Met	Val	Ser	Ser	Asp	Gly
1										10					15

Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
20 25 30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Leu Thr
85 90 95

Phe Pro Pro Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr
195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Arg Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val

420

425

430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
 435 440 445

Val Thr Arg His Asp Tyr Glu Ala Ser Lys
 450 455

<210> 13
 <211> 1377
 <212> DNA
 <213> Arthrobacter sp.

<400> 13
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 gacattctgg tgaaagacgg caaagtgcgc gcaatcagct cggacacaag tgatgttgag 120
 gcgagccgaa ccattgacgc gggtggcaag ttcgtgtatgc cgggcgttgtt cgatgaacat 180
 gcgagccgaa ccattgacgc gggtggcaag ttcgtgtatgc cgggcgttgtt cgatgaacat 240
 tctgcggccg tgggaggcat caccaccatc atcgagatgc cgataacctt cccgcccacc 300
 accactttgg acgccttcct cgaaaagaag aagcaggcgg ggcagcggtt gaaagttgac 360
 ttcgcgcgtct atggcggtgg agtgcgggaa aacctgcggc agatccgcaa aatgcacgac 420
 gcccggcgcag tgggcttcaa gtcaatgtatgc gcagcctcag ttccgggcat gttcgacgcc 480
 gtcagcgcacg gcgaactgtt cgaaatcttc caggagatcg cagcctgtgg ttcagtcgtc 540
 gtggtccatg ccgagaatga aacgatcatt caagcgctcc agaagcagat caaagccgt 600
 ggtcgcaagg acatggccgc ctacgaggca tcccaaccag tttccagga gaacgaggcc 660
 attcagcgtg cgttactact gcagaaagaa gccggctgtc gactgattgt gttcacgtg 720
 agcaaccctg acggggtcga gctgatacat caggcgcaat ccgaggggcca ggacgtccac 780
 tgcgagtcgg gtccgcagta tctgaatatc accacggacg acgcccgaacg aatcggaccg 840
 tatatgaagg tcgcgcccgc cgtccgcgtca gccgagatga acgcccagatt atgggaacaa 900
 cttgagaacg ggctcatcga cacccttggg tcagaccacg gcggacatcc tgcgaggac 960
 aaagaacccg gctggaagga cgtgtggaaa gccggcaacg gtgcgcgtggg ccttgagaca 1020

tccctgccta tcatgctgac caacggagtg aataaaggca ggctatcctt ggaacgcctc 1080
gtcgaggta tgtgcgagaa acctgcgaag ctcttggca tctatccgca gaagggcacg 1140
ctacaggttg gttccgacgc cgatctgctc atcctcgatc tggatattga caccaaagtg 1200
gatgcctcgc agttccgatc cctgcataag tacagccgt tcgacggat gcccgtcacg 1260
ggtgcaccgg ttctgacgat ggtgcgcgga acggtggtgg cagagaaggg agaagttctg 1320
gtcgagcagg gattcggcca gttcgtcacc cgtcacgact acgaggcgtc gaagtga 1377

<210> 14
<211> 458
<212> PRT
<213> Arthrobacter sp.

<400> 14

Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly
1 5 10 15

Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
20 25 30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr
85 90 95

Phe Pro Pro Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Val Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr
195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Ala Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
420 425 430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
435 440 445

Val Thr Arg His Asp Tyr Glu Ala Ser Lys
450 455

<210> 15
<211> 1377
<212> DNA
<213> Arthrobacter sp.

<400> 15
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gacattctgg tgaaagacgg caaagtcgcc gcaatcagct cggacacaag tggatgttgag
gcgagccgaa ccattgacgc gggtggcaag ttcgtgtatgc cgggcgttgtt cgatgaacat 120
gcgagccgaa ccattgacgc gggtggcaag ttcgtgtatgc cgggcgttgtt cgatgaacat
tctgcggccg tgggaggcat caccaccatc atcgagatgc cgttaaccctt cccgcccacc 180
accactttgg acgccttcct cgaaaagaag aagcaggcgg ggcagcgggtt gaaagttgac
300
360

ttcgcgctct	atggcggtgg	agtgccggga	aacctgcccc	agatccgcaa	aatgcacgac	420
gccggcgca	g	gtcaatgatg	gcagcctcag	ttccgggcat	gttcgacgcc	480
gtcagcgac	g	cgaaatcttc	caggagatcg	cagcctgtgg	ttcagtcgtc	540
gtggtccatg	ccgagaatga	aacgatcatt	caagcgctcc	agaagcagat	caaagccgct	600
ggtcgcaagg	acatggccgc	ctacgaggca	tcccaaccag	tttccagga	gaacgaggcc	660
attcagcgtg	cgttactact	gcagaaagaa	gccggctgtc	gactgattgt	gcttcacgtg	720
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tatatgaagg	tcgcgcgc	cgtccgctca	gccgaaatga	acgtcagatt	atggaaacaa	900
cttgagaacg	ggctcatcga	cacccttggg	tcagaccacg	gcggacatcc	tgtcgaggac	960
aaagaacccg	gctggaagga	cgtgtggaaa	gccggcaacg	gtgcgctgg	ccttgagaca	1020
tccctgccta	tgatgctgac	caacggagtg	aataaaggca	ggctatcctt	ggaacgcctc	1080
gtcgaggtga	tgtgcgagaa	acctgcgaag	ctctttggca	tctatccgca	gaagggcacg	1140
ctacaggttg	gttccgacgc	cgatctgctc	atcctcgatc	tggatattga	caccaaagtg	1200
gatgcctcgc	agttccgatc	cctgcataag	tacagccgt	tcgacgggat	gcccgtcacg	1260
ggtgcaccgg	ttctgacgat	ggtgcgcgga	acggtggtgg	cagagaaggg	agaagttctg	1320
gtcgagcagg	gattcggcca	gttcgtcacc	cgtcacgact	acgaggcgtc	gaagtga	1377

<210> 16
 <211> 458
 <212> PRT
 <213> Arthrobacter sp.

 <400> 16

Met	Phe	Asp	Val	Ile	Val	Lys	Asn	Cys	Arg	Met	Val	Ser	Ser	Asp	Gly
1															15

Ile	Thr	Glu	Ala	Asp	Ile	Leu	Val	Lys	Asp	Gly	Lys	Val	Ala	Ala	Ile
															30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Leu Thr
85 90 95

Phe Pro Pro Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr
195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
420 425 430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
435 440 445

Val Thr Arg His Asp Tyr Glu Ala Ser Lys
450 455

<210> 17
<211> 1377
<212> DNA
<213> *Arthrobacter* sp.

<400> 17
atgtttgacg taatagttaa gaactgccgt atgggtgtcca gcgacggaat caccgaggca 60
gacattctgg tgaaagacgg caaagtcgcc gcaatcagct cggacacaag tggatgtttag 120
gcgagccgaa ccattgacgc ggggtggcaag ttcgtgtatgc cggggcgtggc cgatgaacat 180
gcgagccgaa ccattgacgc ggggtggcaag ttcgtgtatgc cggggcgtggc cgatgaacat 240
tctgcggccg tgggaggcat caccaccatc atcgagatgc cgttaaccctt cccgcccacc 300
accactttgg acgccttcctt cgaaaagaag aagcaggcgg ggcagcggtt gaaagttgac 360
ttcgcgcgtct atggcggtgg agtgcgggaa aacctgcccc agatccgcaa aatgcacgac 420
gccggcgcag tgggcttcaa gtcaatgtatgc gcagcctcag ttccggcat gttcgacgcc 480
gtcagcgcacg gcgaaactgtt cgaaatcttc caggagatcg cagcctgtgg ttcagtcgcc 540
gtggtccatg ccgagaatga aacgatcatt caagcgctcc agaagcagat caaagccgct 600
ggtcgcaagg acatggccgc ctacgaggca tcccaaccag tttccagga gaacgaggcc 660
attcagcgtg cgttactact gcagaaagaa gccggctgtc gactgattgt gcttcacgtg 720
agcaaccctg acggggtcga gctgatacat cggcgcaat ccggaggccca ggacgtccac 780
tgcgagtcgg gtccgcagta tctgaatatc accacggacg acgcccgaacg aatcggaccg 840
tatatgaagg tcgcgcgcgc cgtccgctca gccgagatga acgtcagatt atggaaacaa 900
cttgagaacg ggctcatcga cacccttggg tcagaccacg gggacatcc tgtcgaggac 960
aaagaacccg gctggaaagga cgtgtggaaa gccggcaacg gtgcgtggg ccttgagac 1020
tccctgccta tgatgctgac caacggagtg aataaaggca ggctatcctt ggaacgcctc 1080
gtcgaggtga tgtgcgagaa acctgcgaag ctctttggca tctatccgca gaagggcacg 1140
ctacaggttg gttccgacgc cgatctgctc atcctcgatc tggatattga caccaaagtg 1200

gatgcctcgc agttccgatc cctgcataag tacagccgt tcgacggat gcccgtaacg 1260
ggtgtcaccgg ttctgacgat ggtgcgcgga acggtggtgg cagagaaggg agaagttctg 1320
gtcgagcagg gattcggcca gttcgtcacc cgtcacgact acgaggcgta gaagtga 1377

<210> 18
<211> 458
<212> PRT
<213> Arthrobacter sp.

<400> 18

Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly
1 5 10 15

Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
20 25 30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Leu Thr
85 90 95

Phe Pro Pro Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Ala Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr
195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Arg Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
420 425 430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
435 440 445

Val Thr Arg His Asp Tyr Glu Ala Ser Lys
450 455

<210> 19
<211> 1377
<212> DNA
<213> Arthrobacter sp.

<400> 19
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gcgagccgaa ccattgacgc ggggtggcaag ttcgtgtatgc cgggcgttgtt cgtatgaacat 180
gcgagccgaa ccattgacgc ggggtggcaag ttcgtgtatgc cgggcgttgtt cgtatgaacat 240
tctgcggccg tgggaggcat caccaccatc atcgagatgc cgtttacctt cccgcccacc 300
accactttgg acgccttcct cggaaaagaag aagcaggcgg ggcagcgggtt gaaagttgac 360
ttcgcgtct atggcggtgg agtgccggaa aacctgccccg agatccgcaa aatgcacgac 420
gccggcgcag tgggcttcaa gtcaatgatg gcagcctcag ttccgggcat gttcgacgcc 480

gtcagcgacg	gctaactgtt	cgaaatcttc	caggagatcg	cagcctgtgg	ttcagtcgcc	540
gtggtccatg	ccgagaatga	aacgatcatt	caagcgctcc	agaagcagat	caaagccgct	600
ggtcgcaagg	acatggccgc	ctacgaggca	tcccaaccag	tttccagga	gaacgaggcc	660
attcagcgtg	cgttactact	gcagaaagaa	gccggctgtc	gactgattgt	gcttcacgtg	720
agcaaccctg	acggggtcga	gctgatacat	cggcgcaat	ccgagggcca	ggacgtccac	780
tgcgagtcgg	gtccgcagta	tctgaatatc	accacggacg	acgcccgaacg	aatcgaccg	840
tatataagg	tcgcgcgc	cgtccgctca	gccgagatga	acgtcagatt	atggaaacaa	900
cttgagaacg	ggctcatcga	cacccttggg	tcagaccacg	gcggacatcc	tgtcgaggac	960
aaagaacccg	gctggaagga	cgtgtggaaa	gccggcaacg	gtgcgcttgg	ccttgagaca	1020
tccctgccta	tgtgctgac	caacggagtg	aataaaggca	ggctatcctt	ggaacgcctc	1080
gtcgaggtga	tgtgcgagaa	acctgcgaag	ctctttggca	tctatccgca	gaagggcacg	1140
ctacaggttg	gttccgacgc	cgatctgctc	atcctcgatc	tggatattga	caccaaagtg	1200
gatgcctcgc	agttccgatc	cctgcataag	tacagcccgt	tcgacgggat	gcccgtaacg	1260
ggtgcaccgg	ttctgacgat	ggtgcgcgga	acggtggtgg	cagagaaggg	agaagttctg	1320
gtcgagcagg	gattcggcca	gttcgtcacc	cgtcacgact	acgaggcgtc	gaagtga	1377

<210> 20
 <211> 458
 <212> PRT
 <213> *Arthrobacter* sp.

<400> 20

Met	Phe	Asp	Val	Ile	Val	Lys	Asn	Cys	Arg	Met	Val	Ser	Ser	Asp	Gly
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Ile	Thr	Glu	Ala	Asp	Ile	Leu	Val	Lys	Asp	Gly	Lys	Val	Ala	Ala	Ile
					20			25							30

Ser	Ser	Asp	Thr	Ser	Asp	Val	Glu	Ala	Ser	Arg	Thr	Ile	Asp	Ala	Gly
						35			40						45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile

50

55

60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Phe Thr
85 90 95

Phe Pro Pro Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Ala Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr
195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Arg Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
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Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
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Val Thr Arg His Asp Tyr Glu Ala Ser Lys
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